

FIGURE 1A

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hskca3d seq (Our sequence)
Y082603 SEQ (AAD14 sequence)
G16005 SEQ (Genomic sequence in ST5 database)
U69884 SEQ rat SKCa3 (old sequence)
R69884 SEQ rat SKCa3 (revised October 1997)
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[illegible]

FIGURE 1B

hSkca3	CAGGGCCCCCCC	TTCGTCCA	ACTCCACG	CCATCCTCC	ACCCCTTCCTCC	AGGCAAGGCAGCCAGCTCA	700
AAD14	-----C-----	-----T-----	-----	-----	-----	-----	700
G16005	A-----NN-NC-----	-----A-NN-----	-----C-----	-----	-----	-----	373
R69884	-----T-----AAT- -AG-----	-----	-----	-----	-----	-----	415
hSkca3	ATCTCAATGACCACTTGCTTGGCCACTCTCCAAGTTCCACAGCTACAAGTGGGCCTGGCGGAGGCAGCCG	770					770
AAD14	-----T-----	-----	-----	-----	-----	-----	443
G16005	-----	-----	-----	-----	-----	-----	485
R69884	-----G-----C-----T-----	-----	-----	-----	-----	-----	
hSkca3	GCACCGACAGGCCAGCCCCCTGGTGCACCGCGGGACAGCAACCCCTTCACGGAGATCGCCATGAGCTCC	840					840
AAD14	-----	-----	-----	-----	-----	-----	513
G16005	-----	-----	-----	-----	-----	-----	9
U69884	-----	-----	-----	-----	-----	-----	555
R69884	-----G-----G-----T-----A-T-----	-----	-----	-----	-----	-----	
hSkca3	TGCAAGTATAGCGGTGGGGTCATGAAGCCCTCAGCCGCTCAGCGCCTCCCGGAGGAACCTCATCGAGG	910					910
AAD14	-----T-----	-----	-----	-----	-----	-----	583
G16005	-----	-----	-----	-----	-----	-----	79
U69884	-----A-C-----A-----T-----A-----T-----	-----	-----	-----	-----	-----	625
R69884	-----A-C-----A-----T-----A-----T-----	-----	-----	-----	-----	-----	
hSkca3	CCGAGACTGAGGGCCAACCCCTCCAGCTTTTCAGCCCTAGCAACCCCCCGGAGATCGTCATCTCCTCCCG	980					980
AAD14	-----	-----	-----	-----	-----	-----	653
G16005	-----C-----T-----C-----A-----TA-----A-----	-----	-----	-----	-----	-----	149
U69884	-----C-----C-----T-----C-----A-----TA-----A-----	-----	-----	-----	-----	-----	695
R69884	-----C-----C-----T-----C-----A-----TA-----A-----	-----	-----	-----	-----	-----	
hSkca3	GGAGGACAACCATGCCCACCAGACCCTGCTCCATCACCCCTAATGCCACCCACAACCACCAGCATGCCGGC	1,050					1,050
AAD14	-----T-----T-----C-C-T-----	-----	-----	-----	-----	-----	219
U69884	-----T-----T-----C-C-T-----	-----	-----	-----	-----	-----	765
R69884	-----T-----T-----C-C-T-----	-----	-----	-----	-----	-----	
hSkca3	ACCACCGCCAGCAGCACCACCTTCCCCAAGCCAACAAGCGGAAAAACCAAACATTGGCTATAAGCTGG	1,120					1,120
AAD14	-----	-----	-----	-----	-----	-----	289
U69884	-----T-TG-----	-----	-----	-----	-----	-----	835
R69884	-----T-TG-----	-----	-----	-----	-----	-----	
hSkca3	GACACAGGAGGGCCCTGTTTGAAAAGAGAAAGCGACTGAGTGACTATGCTCTGATTTTGGGATGTTTGG	1,190					1,190
AAD14	-----	-----	-----	-----	-----	-----	359
U69884	-G-----	-----	-----	-----	-----	-----	905
R69884	-G-----	-----	-----	-----	-----	-----	
hSkca3	AATTGTTGTTATGGTGATAGAGACCGAGCTCTCTTGGGGTTTGTACTCAAAGGACTCCATGTTTTCGTTG	1,260					1,260
AAD14	-----	-----	-----	-----	-----	-----	429
U69884	-----A-G-----T-----	-----	-----	-----	-----	-----	975
R69884	-----A-G-----T-----	-----	-----	-----	-----	-----	

FIGURE 1C

hSkca3	GCCCTGAAATGCCGTATCAGTCTGTCCACCATCATCCTTTTGGGCTTGATCATCGCCTACCACACACGTG	1,330
AAD14	-----	1,330
U69884	-----T-----T-A-----GC-T-T-----A-G-	499
R69884	-----T-----T-A-----GC-T-T-----A-G-	1,045
hSkca3	GAGTCCAGCTCTTCGTGATCGACAACGACGCGGATGACTGGCGGATAGCCATGACCTACGAGCGCATCCT	1,400
AAD14	-----	1,400
U69884	A--A-----T-----T-GT-A-----T-----	569
R69884	A--A-----T-----T-GT-A-----T-----	1,115
hSkca3	CTACATTAGCCTGGAGATGCTGGTGTACACMAACCAACCATTCCTGGCGAGTACAAGTCTTCTGGGCG	1,470
AAD14	-----	1,470
U69884	-----C-----G-G-C-T--C-----A-----A--	639
R69884	-----C-----G-G-C-T--C-----A-----A--	1,185
hSkca3	GCACGCCCTGGCCTTCTCCTACACACCCCTCCCGGGCGGAGGCCGATGTGGACATCATCCTGTCTATCCCCA	1,540
AAD14	-----	1,540
U69884	-----C--T--A--T--C-----T--T--C-----	709
R69884	-----C--T--A--T--C-----T--T--C-----	1,255
hSkca3	TGTTCCCTGCGCCTGTACCTGATCGCCCGAGTCATGCTGCTACACAGCAAGCTCTTCACCGATGCCTCGTC	1,610
AAD14	-----	1,610
U69884	-----T--A-----T-----G-----A--	779
R69884	-----T--A-----T-----G-----A--	1,325
hSkca3	CCGCAGCATCGGGGCCCTCAACAAGATCAACTTCAACACCCGCTTT GTCAT GAAGACGCTCATGACCA	1,680
AAD14	-----T-----T-----	1,680
U69884	-----A-----A-C-----	849
R69884	-----A-----A-C-----	1,395
hSkca3	TCTGCCCTGGCACTGTGCTGCTCGTGTTCAGCATCTCTCTGTGGATCATTGCTGCCTGGACCGTCCGTGT	1,750
AAD14	-----	1,750
U69884	-----G-----G-----AA-----C-----T--GA-A--	919
R69884	-----G-----G-----G-----C-----T--GA-A--	1,465
hSkca3	CTGTGAAAGGTACCATGACCAGCAGGACGTAAGTAGTAACCTTTCTCGGTGCCATGTGGCTCATCTCCATC	1,820
AAD14	-----	1,820
U69884	-----	989
R69884	-----	1,535
hSkca3	ACATTCCTTTCCATTGGTTATGGGGACATGGTGCCCCACACATACTGTGGGAAAGGTGTCTGTCTCCTCA	1,890
AAD14	-----	1,890
U69884	-----G-----C-----T-----	1,059
R69884	-----G-----C-----T-----	1,605
hSkca3	CTGGCATCATGGGTGCAGGCTGCACTGCCCTTGTGGTGGCCGTGGTGGCCCGAAAGCTGGAACCTACCAA	1,960
AAD14	-----	1,960
U69884	-----C--A--T--T--G--C-----	1,129
R69884	-----C--A--T--T--G--C-----	1,675

FIGURE 1D

hSkca3	AGCGGAGAAGCACGTGCATAACTTCATGATGGACACTCAGCTCACCAAGCGGATCAAGAATGCTGCAGCA	2,030
AAD14	-----CG-----A-----C-----C-C	2,030
U69884	-A-----T-----C-----A-----C-----C-C	1,199
R69884	-A-----T-----C-----A-----C-----C-C	1,745
hSkca3	AATGTCCTTCGGGAAACATGGTTAATCTATAAACACACAAAGCTGCTAAAGAAGATTGACCATGCCAAAG	2,100
U69884	-----C-----C-G-----C-----C-----C-----	1,269
R69884	-----C-----C-G-----C-----C-----C-----	1,815
hSkca3	TGAGGAAACACCAGAGGAAGTTCCTCCAAGCTATCCACCAGTTGAGGAGCGTCAAGATGGAACAGAGGAA	2,170
U69884	-C-----T-----AC-----G-T-----A-----	1,339
R69884	-C-----T-----AC-----G-T-----A-----	1,885
hSkca3	GCTGAGTGACCAAGCCAACACTCTGGTGGACCTTTCCAAGATGCAGAATGTCATGTATGACTTAATCACA	2,240
U69884	-----C-----C-----C-----G-----G-----	1,409
R69884	-----C-----C-----C-----G-----G-----	1,955
hSkca3	GAACTCAATGACCGGAGCGAAGACCTGGAGAAGCAGATTGGCAGCCTGGAGTCGAAGCTGGAGCATCTCA	2,310
U69884	-G-----C-----T-----A-----A-C-----C-----	1,479
R69884	-G-----C-----T-----A-----A-C-----C-----	2,025
hSkca3	CCGCCAGCTTCAACTCCCTGCCGCTGCTCATCGCCGACACCTGCCCCAGCAGCAGCAGCAGCTCCTGTC	2,380
U69884	-A-----T-----C-----A-----A-----A-----G-CA-	1,549
R69884	-A-----T-----C-----A-----A-----A-----G-CA-	2,095
hSkca3	TGCCATCATCGAGGCCCGGGTGTGAGCGTGGCAGTGGGCACCACCCACACCCCAATCTCCGATACGCCC	2,450
U69884	---T--G-G-----CA---T---T---A--T-G---G---TCC---T--C-GC--T	1,619
R69884	---T--G-G-----CA---T---T---A--T-G---G---TCC---T--C-GC--T	2,165
hSkca3	ATTGGGGTCAGCTCCACCTCCTTCCCGACCCCGTACACAAGTTCAAGCAGTTGCTAAATAAATCTCCCCA	2,520
U69884	--C--A-----T-----GAATTCCTA-T-TTC-AG	1,689
R69884	--C--A-----T-----A-----A-----A-----	2,235
hSkca3	CTCCAGAAGCATTAAAAAAAAAAAAA	2,590
R69884	-----	2,305

FIGURE 2A

hskca3.pep (our sequence)
u69884.pep (old rat sequence)
r69884.pep (rat sequence revised in October 1997)
y08263.pep (AAD14 frame 1)
y082631.pep (AAD14 frame 2)
yC82632.pep (AAD14 frame 3)

hSKCa3 R69884 AAD14 F1	Poly Q rpt		MDTSGHFHDSGVGDLDEDPKCPCPSSGDECCCCCCCCCCCCQPPPP ASPAAPQQPLGPSLQPPQLOQQQ	70
	-----E-----		-----S-P-V-----P-L-----	70
	-----		-----SV--VV-----	70
hSKCa3 R69884 AAD14 F1	Poly Q rpt		QCCCCCCCCCCCCQ PHPLSCLAQLCSQPVHPGLLHSSPTAFRAPSSNSTAILHPSSRQGSQNLN	140
	-----		-----QCCCCQAPL-----P-----V-----N-A-----	140
	-----		-----F-----S-----FVQLHRHPP-FLQARQPAQSQ	140
hSKCa3 R69884 AAD14 F2			DHLLGHSPSSSTATSGPGGSRHRQASPLVHRDSDNPFTIAMSSCKYSGGVMPKLSRFSASRRNLIEAET	210
	-----V-----		-----N-L-----P	210
	-----		-----	29
hSKCa3 U69884 R69884 AAD14 F2			EGQFLQLFSPSNPPEIIVISSREDNHAHQTLHHPNATHNHQAGTTASSTTFPKANKRKNQNIQYKLGHR	280
	-----I-----		-----G-----	99
	-----I-----		-----G-----	280
hSKCa3 U69884 R69884 AAD14 F2	S1		RALFEKRKRLSDYALIFGMFGIVVMVIETELSWGLYSKDSMFSLALKCRISLSTIILLGLIIAYHTRGVQ	350
	-----		-----L-----	169
	-----		-----L-----	350
hSKCa3 U69884 R69884 AAD14 F2	S3		LFVIDNDADOWRIAMTYERILYISLEMLVYTNHTIPGEYKFFWAARLAFSYTPSRAEADVDIILSIPMFL	420
	-----G-----		-----CAI-P-----T-----	239
	-----G-----		-----CAI-P-----T-----	420
hSKCa3 U69884 R69884 AAD14 F2	S4		RLYLEIARVMLLHSLFTDASSRSIGALNKINFNTRFVMKTLMTICPGTVLLVFSISLNIIAANTVRVCER	490
	-----		-----M-----	309
	-----		-----CH	490
hSKCa3 U69884 R69884 AAD14 F3	P-reg		YHQDQDVTSNELGAMWLISITFLSIGYGDMPHTYCGKGVCLLTGIMGAGCTALVVAVVARKLELTAKFK	560
	-----		-----	379
	-----		-----	560
hSKCa3 U69884 R69884 AAD14 F3	S6		-----	102
	-----		-----	
	-----		-----	

FIGURE 2B

hSKCa3	HVONFMTDTQLTKRIKNAANVLR	ETWLIYKHTKLLKKIDHAKVRKHQRKFLQAIHQ	LRSVKMEQRKLS	630			
U69884	--H--	-----	--G--	449			
R69884	--H--	-----	--G--	630			
AAD14 F3	--	-----	-----	172			
hSKCa3	QANTLV	DLSKMQNV	MYDLITELNDRSE	DLKQIGSLES	KLHLTASFNSLPLLIADTLR	QQQQQLLSAI	700
U69884	-----	-----	-----	-----	-----	--T-FV	519
R69884	-----	-----	-----	-----	-----	--T-FV	700
hSKCa3	EARGVSV	AVGTTHTPIS	DTPIGV	SSTSF	PTPYTSSSSC		770
U69884	-----I-----	S-A-P--S---	I-----	EF	LI		589
R69884	-----I-----	S-A-P--S---	I-----	-----	-----		770

Figure 3

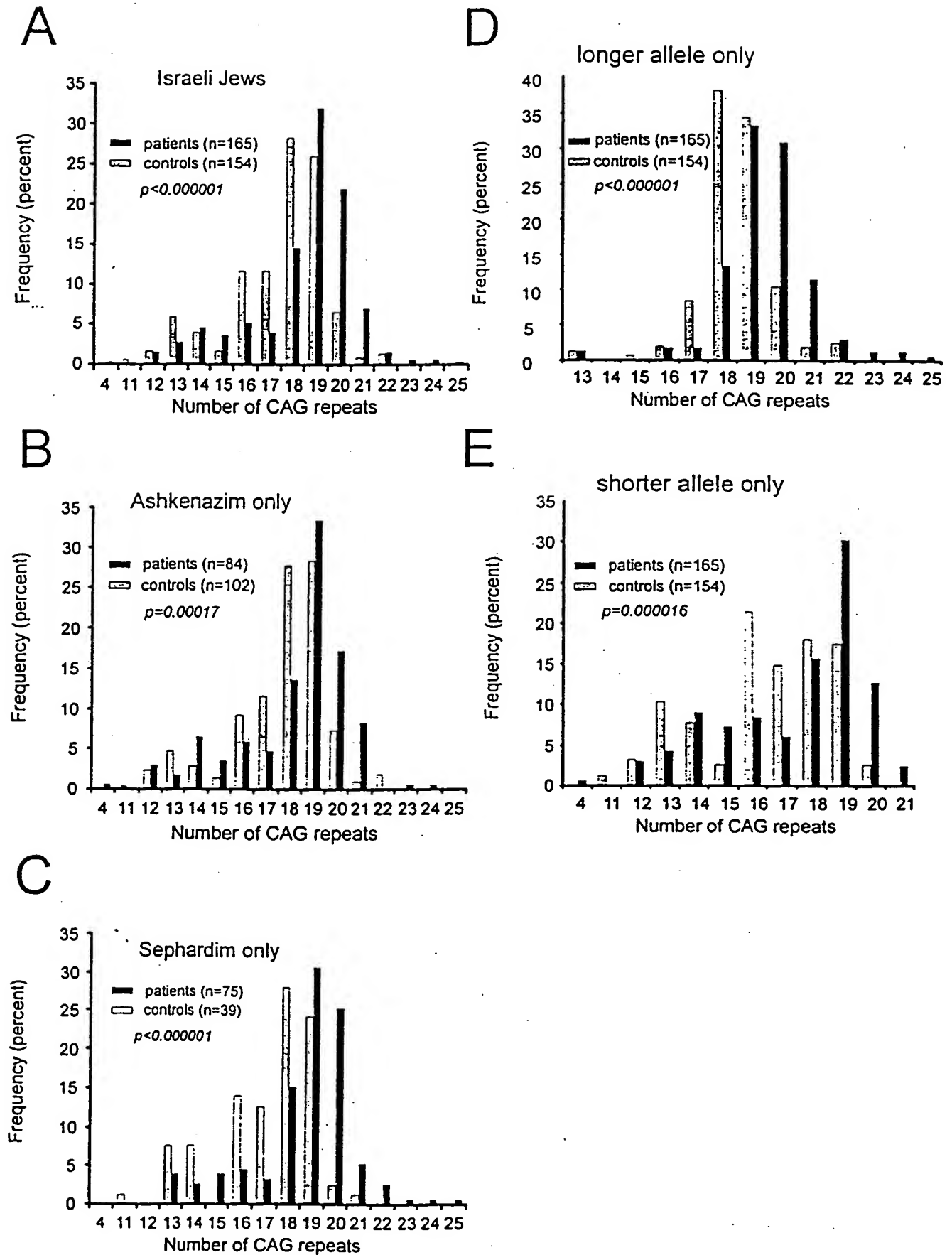


Figure 4

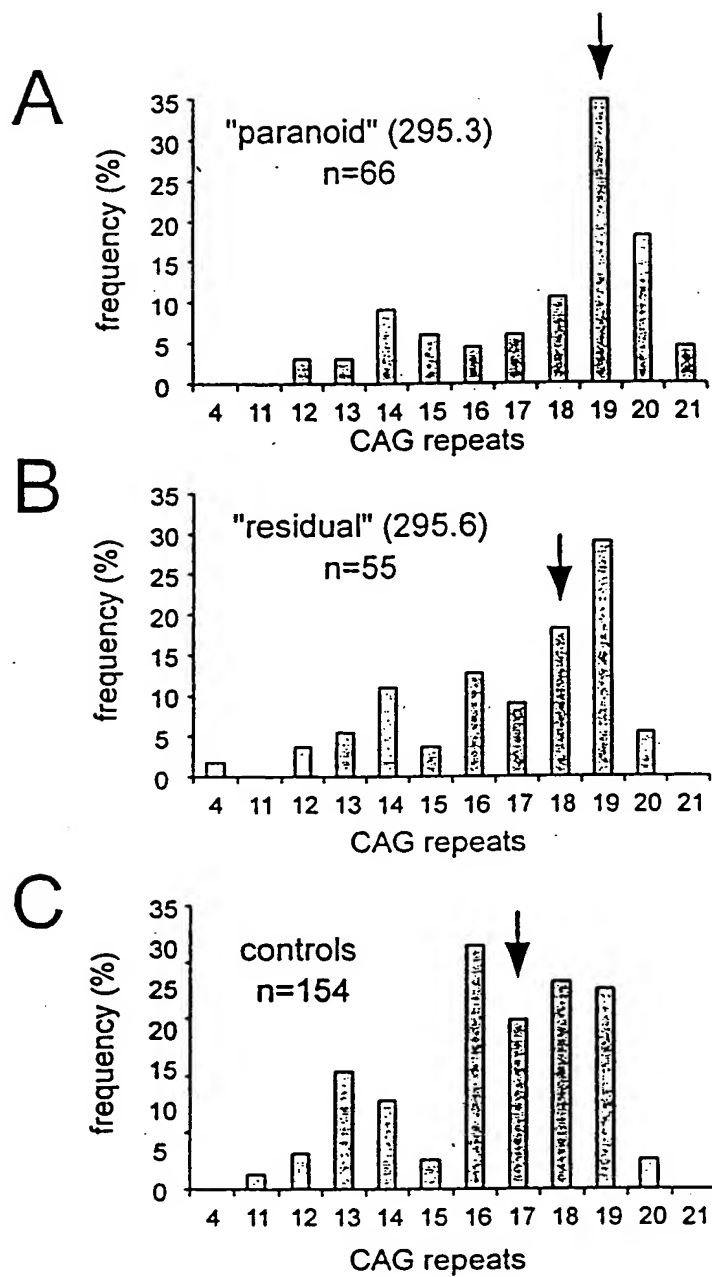


FIGURE 5A

NUCLEOTIDE SEQUENCE AND TRANSLATION OF hKCa3

-286	-280	-270	-260	-250	-240
GCCTCA	CACGCTCCTA	GAGGACCACC	TCCIGAGAGA	GTTCTTTTCAC	CCCCTCTTCT
-230	-220	-210	-200	-190	-180
TTCTCCAAGC	TCCCCTCCTG	CTCTCCCTCC	CTGCCCAATA	CAATGCATTTC	TTGAGTGGCA
-170	-160	-150	-140	-130	-120
GCGTCTGGAC	TCCAGGCAGC	CCCAGAGAAC	CGAAGCAAGC	CAAAGAGAGG	ACTGGAGCCA
-110	-100	-90	-80	-70	-60
AGATACTGGT	GGGGGAGATT	GGATGCCCTGG	CTTCTTTTGA	GGACATCTTT	GGAGCGAGGG
-50	-40	-30	-20	-10	
TGGCTTTGGG	GTGGGGGCTT	GTGCTGCAGG	GAATACAGCC	AGGCCCCAAG	ATG GAC ACT Met Asp Thr
15	30	45	60		
TCT GGG CAC	TTC CAT GAC	TCG GGG GTG	GGG GAC TTG	GAT GAA GAC	CCC AAG TCC
Ser Gly His	Phe His Asp	Ser Gly Val	Gly Asp Leu	Asp Glu Asp	Pro Lys Cys
75	90	105			
CCC TGT CCA	TCC TCT GGG	GAT GAG CAG	CAG CAG CAG	CAG CAG CAG	CAA CAG CAG
Pro Cys Pro	Ser Ser Gly	Asp Glu Gln	Gln Gln Gln	Gln Gln Gln	Gln Gln Gln
120	135	150	165		
CAG CAG CCA	CCA CCG CCA	GCG CCA CCA	GCA GCC CCC	CAG CAG CCC	CTG GGA CCC
Gln Gln Pro	Pro Pro Pro	Pro Ala Pro	Pro Ala Pro	Gln Gln Pro	Leu Gly Pro
180	195	210	225		
TCG CTG CAG	CCT CAG CCT	CCG CAG CTT	CAG CAG CAG	CAG CAG CAG	CAG CAG CAG
Ser Leu Gln	Pro Gln Pro	Pro Gln Leu	Gln Gln Gln	Gln Gln Gln	Gln Gln Gln
240	255	270			
CAG CAG CAG	CAG CAG CCA	CCG CAT CCC	CTG TCT CAG	CTC GCC CAA	CTC CAG AGC
Gln Gln Gln	Gln Gln Pro	Pro His Pro	Leu Ser Gln	Leu Ala Gln	Leu Gln Ser
285	300	315	330		
CAG CCC GTC	CAG CCT GGC	CTG CTG CAC	TCC TCT CCC	ACC GCT TTC	AGG GCC CCC
Gln Pro Val	His Pro Gly	Leu Leu His	Ser Ser Pro	Thr Ala Phe	Arg Ala Pro
345	360	375			
CCT TCG TCC	AAC TCC ACC	GCC ATC CTC	CAC CCT TCC	TCC TCC AGG	CAA GGC AGC
Pro Ser Ser	Asn Ser Thr	Ala Ile Leu	His Pro Ser	Ser Ser Arg	Gln Gly Ser
390	405	420	435		
CTC AAT CTC	AAT GAC CAC	ITG CTT GGC	CAC TCT CCA	AGT TCC ACA	GCT ACA AGT
Leu Asn Leu	Asn Asp His	Leu Leu Gly	His Ser Pro	Ser Ser Thr	Ala Thr Ser
450	465	480	495		
GGG CCT GGC	GGA GGC AGC	CGG CAC CGA	CAG GCC AGC	CCC CTG GTG	CAC CGG CGG
Gly Pro Gly	Gly Gly Ser	Arg His Arg	Gln Ala Ser	Pro Leu Val	His Arg Arg

FIGURE 5B

510										525					540									
GAC	AGC	AAC	CCC	TTC	ACG	GAG	ATC	GCC	ATG	AGC	TCC	TGC	AAG	TAT	AGC	GGT	GGG							
Asp	Ser	Asn	Pro	Phe	Thr	Glu	Ile	Ala	Met	Ser	Ser	Cys	Lys	Tyr	Ser	Gly	Gly							
555										570					585					600				
GTC	ATG	AAG	CCC	CTC	AGC	CGC	CTC	AGC	GCC	TCC	CGG	AGG	AAC	CTC	ATC	GAG	GCC							
Val	Met	Lys	Pro	Leu	Ser	Arg	Leu	Ser	Ala	Ser	Arg	Arg	Asn	Leu	Ile	Glu	Ala							
615										630					645									
GAG	ACT	GAG	GGC	CAA	CCC	CTC	CAG	CTT	TTC	AGC	CCT	AGC	AAC	CCC	CCG	GAG	ATC							
Glu	Thr	Glu	Gly	Gln	Pro	Leu	Gln	Leu	Phe	Ser	Pro	Ser	Asn	Pro	Pro	Glu	Ile							
660										675					690					705				
GTC	ATC	TCC	TCC	CGG	GAG	GAC	AAC	CAT	GCC	CAC	CAG	ACC	CTG	CTC	CAT	CAC	CCT							
Val	Ile	Ser	Ser	Arg	Glu	Asp	Asn	His	Ala	His	Gln	Thr	Leu	Leu	His	His	Pro							
720										735					750					765				
AAT	GCC	ACC	CAC	AAC	CAC	CAG	CAT	GCC	GGC	ACC	GCC	GCC	AGC	AGC	ACC	ACC	TTC							
Asn	Ala	Thr	His	Asn	His	Gln	His	Ala	Gly	Thr	Ala	Ala	Ser	Ser	Thr	Thr	Phe							
780										795					810									
CCC	AAA	GCC	AAC	AAG	CGG	AAA	AAC	CAG	AAC	ATT	GGC	TAT	AAG	CTG	GGA	CAC	AGG							
Pro	Lys	Ala	Asn	Lys	Arg	Lys	Asn	Gln	Asn	Ile	Gly	Tyr	Lys	Leu	Gly	His	Arg							
825										840					855					870				
AGG	GCC	CCG	TTT	GAA	AAG	AGA	AAG	CGA	CTG	AGT	CAC	TAT	GCT	CTG	ATT	TTT	GGG							
Arg	Ala	Pro	Phe	Glu	Lys	Arg	Lys	Arg	Leu	Ser	Asp	Tyr	Ala	Leu	Ile	Phe	Gly							
885										900					915									
ATG	TTT	GGA	ATT	GTT	GTT	ATG	GTG	ATA	GAG	ACC	GAG	CTC	TCT	TGG	GGT	TTG	TAC							
Met	Phe	Gly	Ile	Val	Val	Met	Val	Ile	Glu	Thr	Glu	Leu	Ser	Trp	Gly	Leu	Tyr							
930										945					960					975				
TCA	AAG	GAC	TCC	ATG	TTT	TCG	TTG	GCC	CTG	AAA	TGC	CTT	ATC	AGT	CTG	TCC	ACC							
Ser	Lys	Asp	Ser	Met	Phe	Ser	Leu	Ala	Leu	Lys	Cys	Leu	Ile	Ser	Leu	Ser	Thr							
990										1005					1020					1035				
ATC	ATC	CTT	TTG	GGC	TTG	ATC	ATC	GCC	TAC	CAC	ACA	CGT	GAA	GCC	CAG	CTC	TTC							
Ile	Ile	Leu	Leu	Gly	Leu	Ile	Ile	Ala	Tyr	His	Thr	Arg	Glu	Ala	Gln	Leu	Phe							
1050										1065					1080									
GTG	ATC	GAC	AAT	GGC	GCG	GAT	GAC	TGG	CGG	ATA	GCC	ATG	ACC	TAC	GAG	CGC	ATC							
Val	Ile	Asp	Asn	Gly	Ala	Asp	Asp	Trp	Arg	Ile	Ala	Met	Thr	Tyr	Glu	Arg	Ile							
1095										1110					1125					1140				
CTG	TAC	ATC	AGC	CTG	GAG	ATG	CTG	GTG	TGC	GCC	ATC	CAC	CCC	ATT	CCT	GGC	GAG							
Leu	Tyr	Ile	Ser	Leu	Glu	Met	Leu	Val	Cys	Ala	Ile	His	Pro	Ile	Pro	Gly	Glu							
1155										1170					1185									
TAC	AAG	TTC	TTC	TGG	ACG	GCT	CGC	CTG	GCC	TTC	TCC	TAC	ACA	CCC	TCC	CGG	GCG							
Tyr	Lys	Phe	Phe	Trp	Thr	Ala	Arg	Leu	Ala	Phe	Ser	Tyr	Thr	Pro	Ser	Arg	Ala							

FIGURE 5C

1200 1215 1230 1245
 GAG GCC GAT GTG GAC ATC ATC CTG TCT ATC CCC ATG TTC CTG CGC CTG TAC CTG
 Glu Ala Asp Val Asp Ile Ile Leu Ser Ile Pro Met Phe Leu Arg Leu Tyr Leu

1260 1275 1290 1305
 ATC GCC CGA GTC ATG CTG CTG CAC AGC AAG CTC TTC ACC GAT GCC TCG TCC CGC
 Ile Ala Arg Val Met Leu Leu His Ser Lys Leu Phe Thr Asp Ala Ser Ser Arg

1320 1335 1350
 AGC ATC GGG GCC CTC AAC AAG ATC AAC TTC AAC ACC CGC TTT GTC ATG AAG ACG
 Ser Ile Gly Ala Leu Asn Lys Ile Asn Phe Asn Thr Arg Phe Val Met Lys Thr

1365 1380 1395 1410
 CTC ATG ACC ATC TGC CCT GGC ACT GTG CTG CTC GTG TTC AGC ATC TCT CTG TGG
 Leu Met Thr Ile Cys Pro Gly Thr Val Leu Leu Val Phe Ser Ile Ser Leu Trp

1425 1440 1455
 ATC ATT GCT GCC TGG ACC GTC CGT GCC TGT GAA AGG TAC CAT GAC CAG CAG GAC
 Ile Ile Ala Ala Trp Thr Val Arg Ala Cys Glu Arg Tyr His Asp Gln Gln Asp

1470 1485 1500 1515
 GTA ACT AGT AAC TTT CTG GGT GCC ATG TGG CTC ATC TCC ATC ACA TTC CTT TCC
 Val Thr Ser Asn Phe Leu Gly Ala Met Trp Leu Ile Ser Ile Thr Phe Leu Ser

1530 1545 1560 1575
 ATT GGT TAT GGG GAC ATG GTG CCC CAC ACA TAC TGT CGG AAA GGT GTC TGT CTC
 Ile Gly Tyr Gly Asp Met Val Pro His Thr Tyr Cys Gly Lys Gly Val Cys Leu

1590 1605 1620
 CTC ACT GGC ATC ATG GGT GCA GGC TGC ACT GCC CTT GTG GTG GCC CTG GTG GCC
 Leu Thr Gly Ile Met Gly Ala Gly Cys Thr Ala Leu Val Val Ala Val Val Ala

1635 1650 1665 1680
 CGA AAG CTG GAA CTC ACC AAA GCG GAG AAG CAC GTT CAT AAC TTC ATG ATG GAC
 Arg Lys Leu Glu Leu Thr Lys Ala Glu Lys His Val His Asn Phe Met Met Asp

1695 1710 1725
 ACT CAG CTC ACC AAG CGG ATC AAG AAT GCT GCA GCC AAT GTC CTT CGG GAA ACA
 Thr Gln Leu Thr Lys Arg Ile Lys Asn Ala Ala Ala Asn Val Leu Arg Glu Thr

1740 1755 1770 1785
 TGG TTA ATC TAT AAA CAC ACA AAG CTG CTA AAG AAG ATT GAC CAT GCC AAA GTG
 Trp Leu Ile Tyr Lys His Thr Lys Leu Leu Lys Lys Ile Asp His Ala Lys Val

1800 1815 1830 1845
 AGG AAA CAC CAG AGG AAG TTC CTC CAA GCT ATC CAC CAG TTG AGG AGC GTC AAG
 Arg Lys His Gln Arg Lys Phe Leu Gln Ala Ile His Gln Leu Arg Ser Val Lys

1860 1875 1890
 ATG GAA CAG AGG AAG CTG AGT GAC CAA GCC AAC ACT CTG GTG GAC CTT TCC AAG
 Met Glu Gln Arg Lys Leu Ser Asp Gln Ala Asn Thr Leu Val Asp Leu Ser Lys

FIGURE 5D

1905 1920 1935 1950
 ATG CAG AAT GTC ATG TAT GAC TTA ATC ACA GAA CTC AAT GAC CGG AGC GAA GAC
 Met Gln Asn Val Met Tyr Asp Leu Ile Thr Glu Leu Asn Asp Arg Ser Glu Asp

 1965 1980 1995
 CTG GAG AAG CAG ATT GGC AGC CTG GAG TCG AAG CTG GAG CAT CTC ACC GCC AGC
 Leu Glu Lys Gln Ile Gly Ser Leu Glu Ser Lys Leu Glu His Leu Thr Ala Ser

 2010 2025 2040 2055
 TTC AAC TCC CTG CCG CTG CTC ATC GCC GAC ACC CTG CGC CAG CAG CAG CAG CAG
 Phe Asn Ser Leu Pro Leu Leu Ile Ala Asp Thr Leu Arg Gln Gln Gln Gln Gln

 2070 2085 2100 2115
 CTC CTG TCT GCC ATC ATC GAG GCC CGG GGT GTC AGC CTG GCA GTG GGC ACC ACC
 Leu Leu Ser Ala Ile Ile Glu Ala Arg Gly Val Ser Val Ala Val Gly Thr Thr

 2130 2145 2160
 CAC ACC CCA ATC TCC GAT AGC CCC ATT GGG GTC AGC TCC ACC TCC TTC CCG ACC
 His Thr Pro Ile Ser Asp Ser Pro Ile Gly Val Ser Ser Thr Ser Phe Pro Thr

 2175 2190 2205 2220
 CCG TAC ACA AGT TCA AGC AGT TGC TAA ATA AAT CTC CCC ACT CCA GAA GCA TTA
 Pro Tyr Thr Ser Ser Ser Ser Cys *

 2235
 AAA AAA AAA AAA

FIGURE 6

Alignment of cDNA and Genomic sequence of hKCa3
showing intron/exon boundary

	1140	1150	1160	1170	1180	1190
hKCa3f.seq	ACTGAGTGACTATGCTCTGATTTTTGGGATGTTTGAATTGTTGTTATGGTGATAGAGA					
B1-1395.SEQ	ACTGAGTGACTATGCTCTGATTTTTGGGATGTTTGAATTGTTGTTATGGTGATAGAGA					
	1200	1210	1220	1230	1240	1250
hKCa32f.seq	CCGAGCTCTCTTGGGGTTTGTACTCAAAGGACTCCATGTTTTTCGTTGGCCCTGAAATGCC					
B1-1395.SEQ	CCGAGCTCTCTTGGGGTTTGTACTCAAAGGTAGGGGCTGTGGTTTCTCTTTATACCTTGA					
			↑	begin Intron 1		
B1-1395.SEQ	ACAAAAGGAATATGTAGGTAGCAAGAGAGGGATTGAGAGAGGGGGATATTGAGAGAGAGA					
B1-1395.SEQ	GAGAGAGAGAGAGAGAGAGATTGAGAGATTGGGAGGGAGACTGGGAGAGAGAGGTGGTGG					
B1-1395.SEQ	TGGTGGTGAGAGGCGCTTGCTCAGTTATAT					

FIGURE 7

Genomic map of hKCa3, first exon

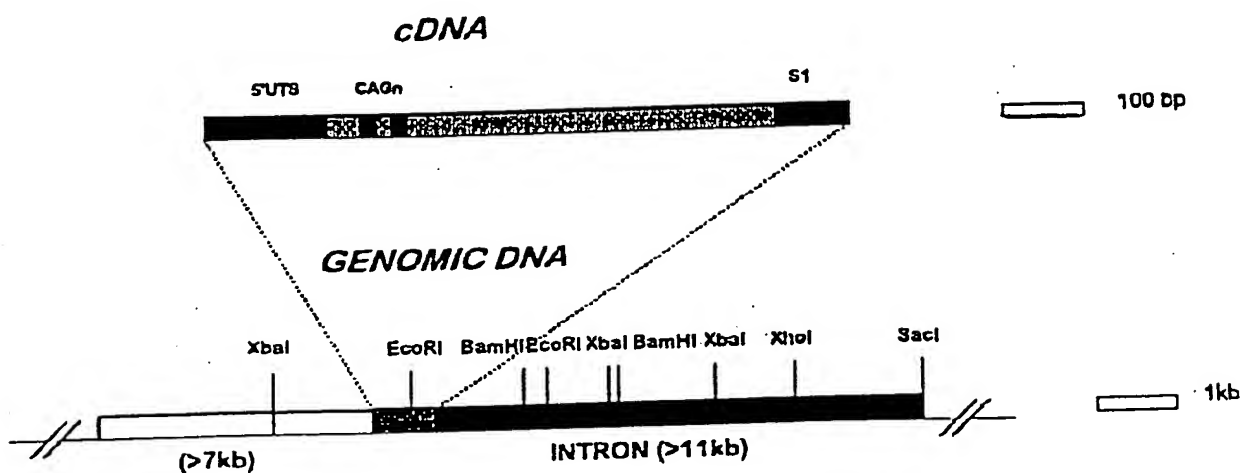


FIGURE 8

5' Flanking/Untranslated sequence of hKCa3/KCNN3

CCC	TTG	AAC	ACG	AGG	CGT	TAG	ACA	CTC	CAG	TCC	ATG	36
GTA	GGT	TAG	TTT	TTA	TCC	NCC	GGG	GTG	TTA	GAA	ACG	72
TGG	GNA	TCC	CCC	CCT	GGT	TCT	GTG	ACC	TTT	GAC	GTT	108
GTT	ACT	CAA	CAC	CTT	TTA	AGC	ATC	AGG	CTT	TGT	AAA	144
TTG	AGA	CCA	TAC	TGG	CCC	ACC	TCC	TTG	GGT	GTT	TGA	180
AGA	CTG	TAT	CCG	GAT	AAT	ATA	TGT	GAA	ACN	ACC	TAT	216
CGT	AAA	CCC	TGG	TGG	TTA	ATA	AAT	GTT	TGC	CTT	CCC	252
CTC	CGT	CTG	CCC	CCT	TCA	TCC	AGG	GTG	CAC	ACC	TCC	288
CCT	CCT	TCG	GAG	GCC	CTC	TGT	CCC	TCC	TCC	CCA	TCG	324
CCC	AGC	GTG	AGC	GAA	CAT	CCC	TTA	TCG	CCG	TGG	GCT	360
TAA	GGG	TTG	TGG	CCA	TAC	CTG	TCA	GAG	GAA	AGA	GGA	396
CAG	CGG	CTC	AGC	TCC	GGG	GTG	GGG	GAG	CAA	AAA	CTA	432
CAG	TTC	CCA	GTC	CTC	GCT	GCG	CCG	CCA	CTG	GGG	CCG	468
GAG	CCC	AGG	ACG	CCA	GGC	CCC	TCC	TCT	GGG	GAG	GAG	504
CCT	ATG	CGG	GGG	GCG	GAG	CTA	GGA	GGA	GGT	TGG	AGA	540
GTT	AAG	CCA	AGC	CAA	TGA	GAC	CAG	CTG	CTA	ATA	AGT	576
GGG	CTT	GGC	TTA	CAA	TGT	AAC	AGT	GGC	AGG	AGG	AGG	612
CGA	GCG	AAG	CTA	TTG	AGC	CAG	CGA	GGA	GTG	AAG	TGA	648
GCC	TGG	CCT	CAC	ACG	CTC	CTA	GAG	GAC	CAC			684

↑
start of overlap with HSKCa3 cDNA sequence